

FIG. 1A

TCGATAGGTA	CCCACTATAG	GGCACGCGTG	GTCGACGGCC	CGGGCTGGTC	50
1					
TGGCAACTTC	AAGTGTGGGC	CTTTCAGACC	GGCATCATCA	GTGTTACGGG	100
51					
GAAGTCACTA	GGAATGCAGA	ATTGATTGAG	CACGGTGGCT	CACACCTGTA	150
101					
ATCCCAACAC	TCTGGGAGGC	CAAGGCAGGT	GGATCACTTG	TGGTCAGGAG	200
151					
TTTGAGACCA	GCCTGGCCAA	CATGGTGAAA	CCTCATCTCT	ACTAAAAATA	250
201					
CAAAAATTAG	CTGGGAATGG	TGGCACATGC	CTATAATCCC	AGTTACTCAG	300
251					
GAGGCTGAGG	CAGGAGAATC	ATTTGAACCT	GGGAGGCAGA	GGTTGCAGTG	350
301					
AGCCGAGATC	ACGCCACTGC	ACTCCAGCCT	GGGTGACACA	GCGAGACTCT	400
351					
GTCTCAAAAA	AAAAAAAATG	CAGAATTTCA	GGCTTCACCC	CAGACCCACT	450
401					
GCATGACTGC	ATGAGAAGCT	GCATCTTAAC	AAGATCCCTG	GTAATTCATA	500
451					
CGCATATTAA	ATTTGGAGAT	GCACTGGCGT	AAGACCCTCC	TACTCTCTGC	550
501					
TTAGGCCCAT	GAGTTCTTCC	TTTACTGTCA	TTCTCCACTC	ACCCCAAAC	600
551					
TTGAGCCTAC	CCTTCCCACC	TTGGCGGTAA	GGACACAACC	TCCCTCACAT	650
601					
TCCTACCAGG	ACCCTAAGCT	TCCCTGGGAC	TGAGGAAGAT	AGAATAGTTC	700
651					
GTGGAGCAAA	CAGATATACA	GCAACAGTCT	CTGTACAGCT	CTCAGGCTTC	750
701					

FIG. 1B

TGGAAGTTCT	ACAGCCTCTC	CCGACAAAGT	ATTCCACTTT	CCACAAGTAA	800
751					
CTCTATGTGT	CTGAGTCTCA	GTTTCCACTT	TTCTCTCTCT	CTCTCTCTCT	850
801					
CAACTTTCTG	AGACAGAGTT	TCACTTAGTC	GCCCAGGCTG	GAGTGCAGGG	900
851					
GCACAATCTC	GGCTCACTGC	AACCTCCACC	TCCTGGGTTC	AAGTGTTTCT	950
901					
CCTGTCTCAG	CCTCCCGAGT	AGCTGGGATT	ACAGGCACAC	ACCACCGCGT	1000
951					
TAGTTTTTGT	ATTTTTGGTA	GAGATGGTGT	TTCGCCATAT	TGGCCAGGCT	1050
1001					
GATCTCGAAC	TCCTGACCTC	AGGTGATCCG	CCCACCTCGG	CCTCCCAAAG	1100
1051					
TGCTGGGATT	ACAGGCATGA	GCCACCACGC	CCGGCTGATC	TCTTTTCTAT	1150
1101					
TTTAATAGAG	ATCAAACCTCT	CTGTGTTGCC	TAGGCTGGTC	TTGAACTCCT	1200
1151					
GGCCTCGAGT	GATCCTCCCA	CCTTGGCCTC	CCAAAGTGTT	GAGATTACAG	1250
1201					
GCATGAGCCA	CTGTGCCTGG	CCTCAGTTCT	ACTACAAAAG	GAAGCCAGTA	1300
1251					
CCAGCTACCA	CCCAGGGTGG	CTGTAGGGCT	ACAATGGAGC	ACACAGAACC	1350
1301					
CCTACCCAGG	GCCCGBAAGA	AGCCCCGACT	CCTCTCCCCT	CCCTCTGCCC	1400
1351					
AGAACTCCTC	CGCTTCTTTC	TGATGTAGCC	CAGGGCCGGA	GGAGGCAGTC	1450
1401					
AGGGAAGTTC	TGTCTCTTTT	TCATGTTATC	TTACGAGGTC	TCTTTTCTCC	1500
1451					

FIG. 1C

ATTCTCAGTC 1501	CAACAAATGG	TTGCTGCCCCA	AGGCTGACTG	TGCCCACCCC 1550
CAACCCCTGC 1551	TGGCCAGGGT	CAATGTCTGT	CTCTCTGGTC	TCTCCAGAAG 1600
TCTTCCATGG 1601	CCACCTTCGT	CCCCACCCTC	CAGAGGAATC	TGAAACCGCA 1650
TGTGCTCCCT 1651	GGCCCCCACA	GCCCCCTGCCT	CTCCCAGAGC	AGCAGTACCT 1700
AAGCCTCAGT 1701	GCACTCCAAG	AATTGAAACC	CTCAGTCTGC	TGCCCCTCCC 1750
CACCAGAATG 1751	TTTCTCTCCC	ATTCTTACCC	ACTCAAGGCC	CTTTCAGTAG 1800
CCCCTTGGAG 1801	TATTCTCTTC	CTACATATCA	GGGCAACTTC	CAAACCTCATC 1850
ACCCTTCTGA 1851	GGGGTGGGGG	AAAGACCCCC	ACCACATCGG	GGGAGCAGTC 1900
CTCCAAGGAC 1901	TGGCCAGTCT	CCAGATGCCC	GTGCACACAG	GAACACTGCC 1950
TTATGCACGG 1951	GAGTCCCAGA	AGAAGGGGTG	ATTTCTTTCC	CCACCTTAGT 2000
TACACCATCA 2001	AGACCCAGCC	AGGGCATCCC	CCCTCCTGGC	CTGAGGGCCA 2050
GCTCCCCATC 2051	CTGAAAAACC	TGTCTGCTCT	CCCCACCCCT	TTGAGGCTAT 2100
AGGGCCCAAG 2101	GGGCAGGTTG	GACTGGATTG	CCCTCCAGCC	CCTCCCGCCC 2150
CCAGGACAAA 2151	ATCAGCCACC	CCAGGGGCAG	GGCCTCACTT	GCCTCAGGAA 2200
CCCCAGCCTG 2201	CCAGCACCTA	TTCCACCTCC	CAGCCCAGCA 2239	

[illegible]

CTCGAGGATCTCGGCCCTCTTTCTGCACTCCTTGTCCTAAATCATTTTTCAT
1 50

ATCTTGCTAGACCTCAGTTTGTAGAGAAACGAACCTTCTCATTTTCAAGTT
51 100

GAAAAAAAAAAGAGGTTCAAAGTGGCTCACTCAAAGTTACAAGCCAACAC
101 150

TCACCACTACGAGTACAATGGCCACCATTAGTGCTGGCATGCCCCAGGAG
151 200

ACAGGCATGCATATTATTCTAGATGACTGGGAGGCAGAGGGGTGGCCTAG
201 250

TGAGGTCAGACTGTGGACAGATCAGGCAGATGTGGGTTCTGATCCCAATT
251 300

CCTCAGGCCCGCAGAACTACTGTGGTTCAAGAAGGGGACAAAAGGACTGCA
301 350

GTCCGGAACAGGAGGTCCATTTGAGAGCTGACTGAGCAGAAGAGGAAAGT
351 400

GAAGAACTTCTGGGGCAAGAGCTTACCCTACTTTACAGCTTTGTTGTCTT
401 450

CTTTACTCCAGGGGCGTCCCTGGTACTCAGTAAATGTCTGTTGGCTTGAG
451 500

GAACATATGTGTAAGGAGGAAGGAGAGGGAACCTGAGGGAGTTAAGACTC
501 550

AAGAATCAATCAAGGAGAGGACAGCAGAGAAGACAGGGTTTGGGAGAGAG
551 600

ACTCCAGACATTGGCCCTGGTTCCCTTCTTGCCACTGTGAAACCCTCCA
601 650

GAGGAACTGAGTGCTGTGGCTTTAAATGATCTCAGCACTGTCAGTGAAGC
651 700

GCTCTGCTCAAAGAGTTATCCTCTTGCTCCTGTGCCGGGGCCTCCCCCTC
701 750

CTCTCAGCTCCCAAACCCTTCTCAGCCACTGTGATGGCATAATTAGATGC
751 800

GAGAGCTCAGACCGTCAGGTCTGCTCCAGGAACCACCCATTTTCCCCAAC
801 850

FIG. 2B

CCCAGAGAAAGGTCCTAGTGGAAGTGGGGGCCACTGAAGGGCTGATGG
851 900

GGTTCTGTCCTTTCCCCCATGCTGGGTGGACTTAAAGTCTGCGATGTGTG
900 950

TAGGGGGTAGAAGACAACAGAACCTGGGGGCTCCGGCTGGGAGCAGGAGG
951 1000

AACTCTCACCAGACGATCTCCAAATTTACTGTGCAATGGACGATCAGGAA
1001 1050

ACTGGTTCAGATGTAGCTTCTGATACAGTGGGTCTGAGGTAAAACCCGAA
1051 1100

ACTTAATTTCTTCAAAAATTTAAAGTTGCATTTATTATTTTATATGTGT
1101 1150

GCCCATATGTGTGCCACAGTGTCTATGTGGAGGTCAGAGGGCAAGTTGTG
1151 1200

GGCATTGGCTCTCTCCTTTTCATAATGTGGCTTCTGGGGACCAAAATGTCA
1201 1250

GGCATGGTGGCAAGAGCTTTTACCTGTTGAGCCATCTCATGGTTTCGTAA
1251 1300

AACTTCCTATGACGCTTACAGGTAACGCAGAGACACAGACTCACATTTGG
1301 1350

AGTTAGCAGATGCTGTATTGGTGTAACACTCATAACACAGACACACACAC
1351 1400

ATACTCATAACACACACACACTTATCACATGCACACACATACTCGTA
1401 1450

TACACACAGACACACACACATGCACTCTCACATTCACATATTCATACACA
1451 1500

TCCACACACACACTCATCCACACACACAGACACACATACTCATCCACACA
1501 1550

CACACACACATACTCATAACACACACAGACACACATACTCATAACACA
1551 1600

CACACAGACACACACATATAATCATAACACACAGACACACTCATAACATG
1601 1650

TGCACACACACACTCATCCACACACACACACTCATAACACACACACTCA
1651 1700

FIG: 2C

TACACACACACACTCATAACACACACACGAGGTTTTTCTCAGGCTGCCT
1701 1750

TTGGGTGGAGACTGGAAGTCTCTGTTTTTCAGCTCCTTGGCTTTTTG
1751 1800

TCCCTTTAGATGAGATCTCCTCCTCACTTTACACACAGAAAGATCACACA
1801 1850

CGAGGGAGAACTGGCGGTGCGGAAGAGGGCTACACGGTAGGGTGTCAGGG
1851 1900

TCAGGAGATCTTCCTGGCAAGTCTCAAACCTCCACATAGCACAGTGTTTA
1901 1950

CGTGAGGATTTAGGAGGAATCAGGAAGAGGATTGGTTTACTGCAGAGCAG
1951 2000

ACCATATAGGTCCACTCCTAAGCCCCATTTGAAATTAGAAGTGAGACAGT
2001 2050

GTGGGATAAAAAGAGCAGATCTCTGGTCACATTTTTTAAAGGGATATGAGG
2051 3000

GTCCTGTGCCTTTAAGCCTTCCCATCTCCCTCCAATCCCCCTCACCTTC
2101 2150

CCCACCCTAACCCTCCCCAGGTTTCTGGAGGAGCAGAGTTGCGTCTTCTC
2151 2200

CCTGCCCTGCCGAGCTGCTCACTGGCTGCTCTAGAGGCTGTGCTTTGCGG
2201 2250

TCTCCATGGAAACCATTAGTTGCTAAGCAACTGGAGCATCATCTGTGCTG
2251 2300

AGCTCAGGTCCTATCGAGTTCACCTAGCTGAGACACCCACGCCCCCTGCAG
2301 2350

CCACTTTGCAGTGACAAGCCTGAGTCTCAGGTTCTGCATCTATAAAAACG
2351 2400

AGTAGCCTTTTACAGGAGGGCATGCAGAGCCCCCTGGCCAGCGTCTAGAGGA
2401 2450

GAGGTGACTGAGTGGGGCCATGTCACTCGTCCATGGCTGGAGAACCCTCCA
2451 2500

TCAGTCTCCCAGTTAGCCTGGGGCAGGAGAGAACCAGAGGAGCTGTGGCT
2501 2550

FIG. 2D

GCTGATTGGATGATTACGTACCCAATCTGTTGTCCCAGGCATCGAACCC
2551 2600

CAGAGCGACCTGCACACATGCCACCGCTGCCCCGCCCTCCACCTCCTCTG
2601 2650

CTCCTGGTTACAGGATTGTTTTGTCTTGAAGGGTTTTGTTGTTGCTACTT
2651 2700

TTTGCTTTGTTTTTTCTTTTTTAACATAAGGTTTCTCTGTGTAGCCCTAG
2701 2750

CTGTCCTGGAACCTCACTCTGTAGACCAGGCTGGCCTCAAACCTCAGAAATC
2751 2800

CACCTTCCTCCCAAGTGCTGGGATTAAAGGCATTCGCACCATCGCCCAGC
2801 2850

CCCCGGTCTTGTTTCCTAAGGTTTTCTGCTTTACTCGCTACCCGTTGCA
2851 2900

CAACCGCTTGCTGTCCAAGTCTGTTTGTATCTACTCCACCGCCCACTAGC
2901 2950

CTTGCTGGACTGGACCTACGTTTACCTGGAAGCCTTCACTAACTTCCCTT
2951 3000

GTCTCCACCTTCTGGAGAAATCTGAAGGCTCACACTGATACCTCCGCTT
3001 3050

CTCCCAGAGTCGCAGTTTCTTAGGCCTCAGTTAAATACCAGAATTGGATC
3051 3100

TCAGGCTCTGCTATCCCCACCCTACCTAACCAACCCCCTCCTCTCCCATC
3101 3150

CTTACTAGCCAAAGCCCTTTCAACCCTTGGGGCTTTTCCTACACCTACAC
3151 3200

ACCAGGGCAATTTTAGAACTCATGGCTCTCCTAGAAAACGCCTACCTCCT
3201 3250

TGGAGACTGACCCTCTACAGTCCAGGAGGCAGACACTCAGACAGAGGAAC
3251 3300

TCTGTCCTTCAGTCGCGGGAGTTCCAGAAAGAGCCATACTCCCCTGCAGA
3301 3350

GCTAACTAAGCTGCCAGGACCCAGCCAGAGCATCCCCCTTTAGCCGAGGG
3351 3400

[illegible]

AGCCTGTCAGCACCTGTTCCAGGATCCAGTCCCAGCGCAGTA
3551 3592

Figure 3A

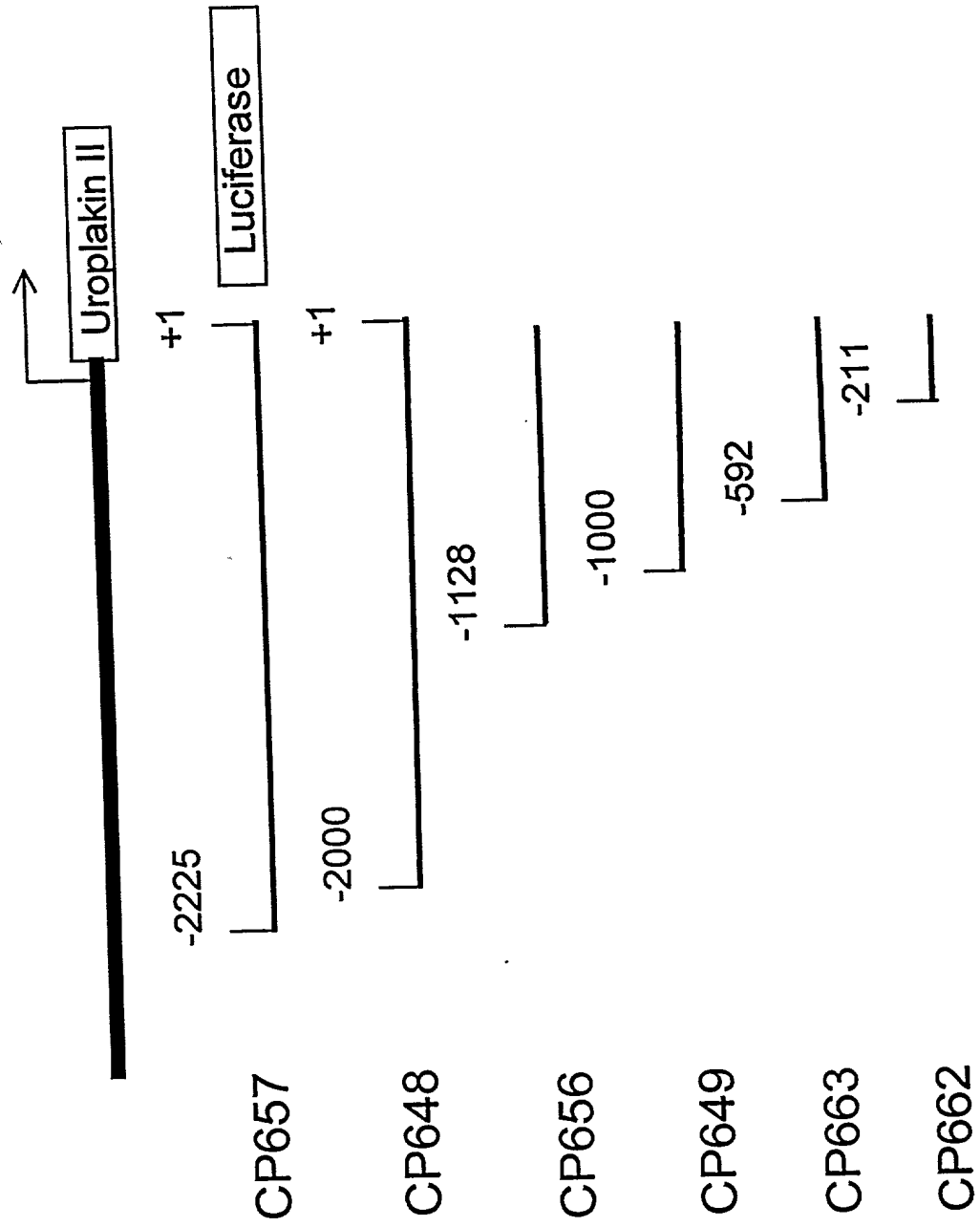


Figure 3B

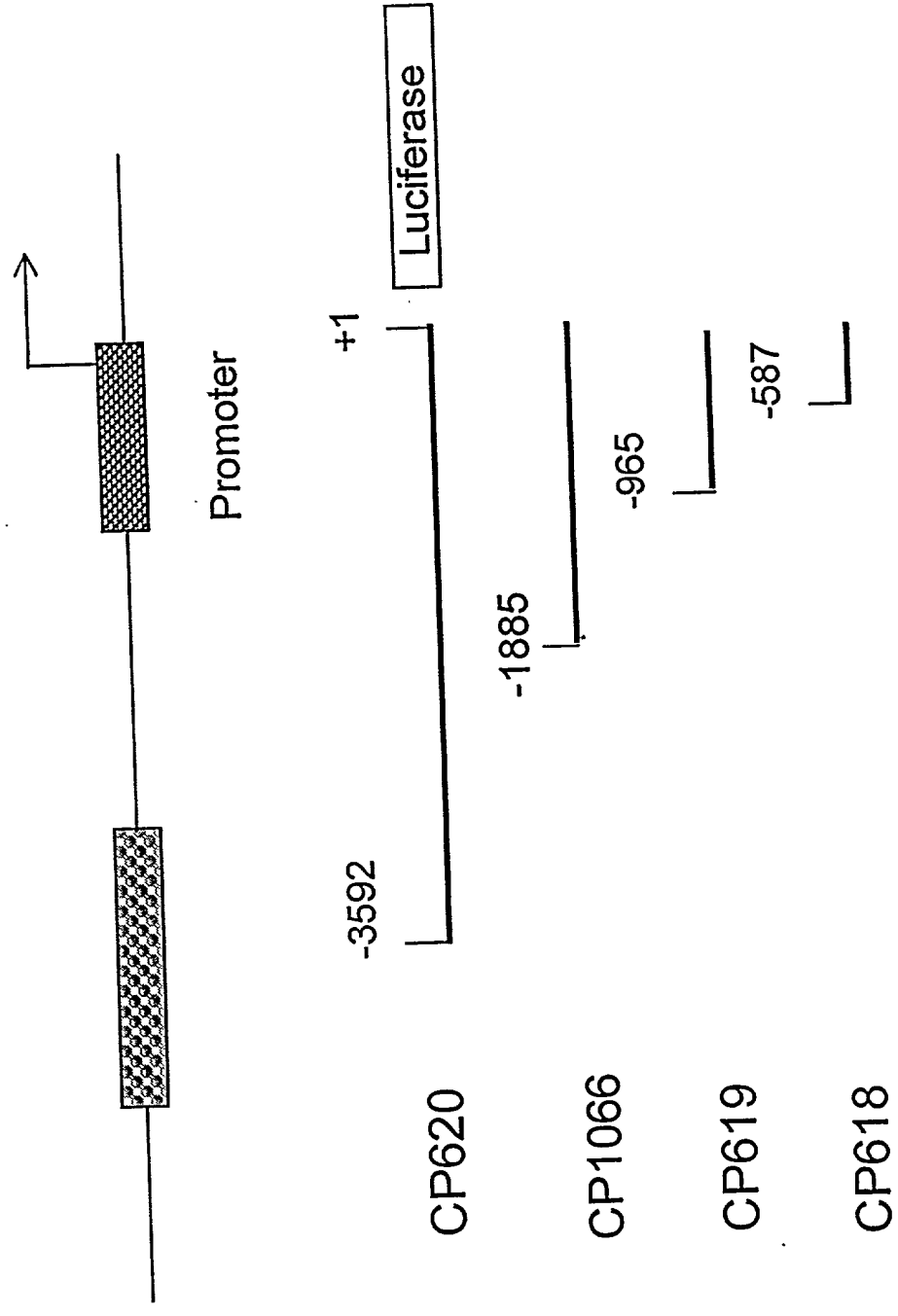


Figure 4A

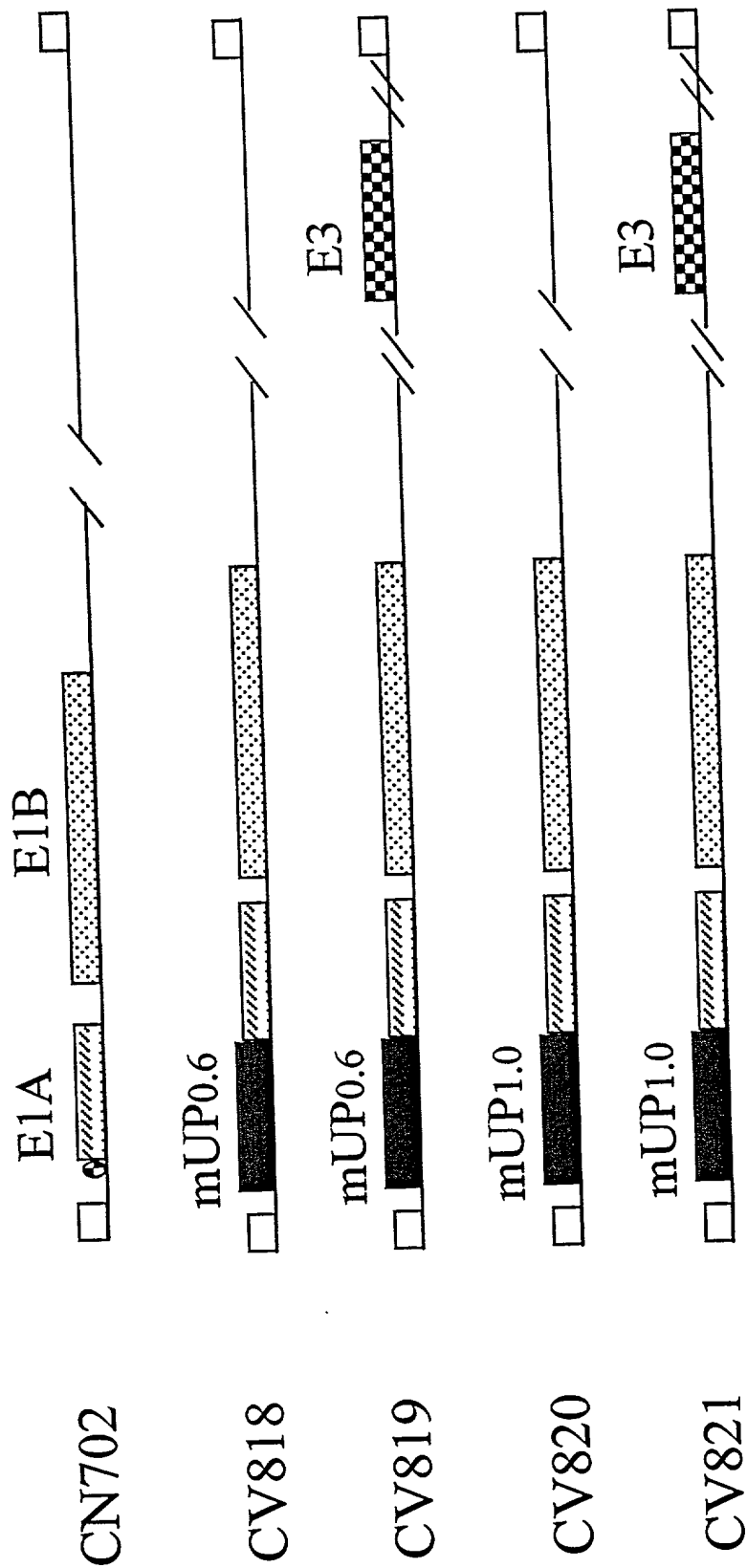


Figure 4B

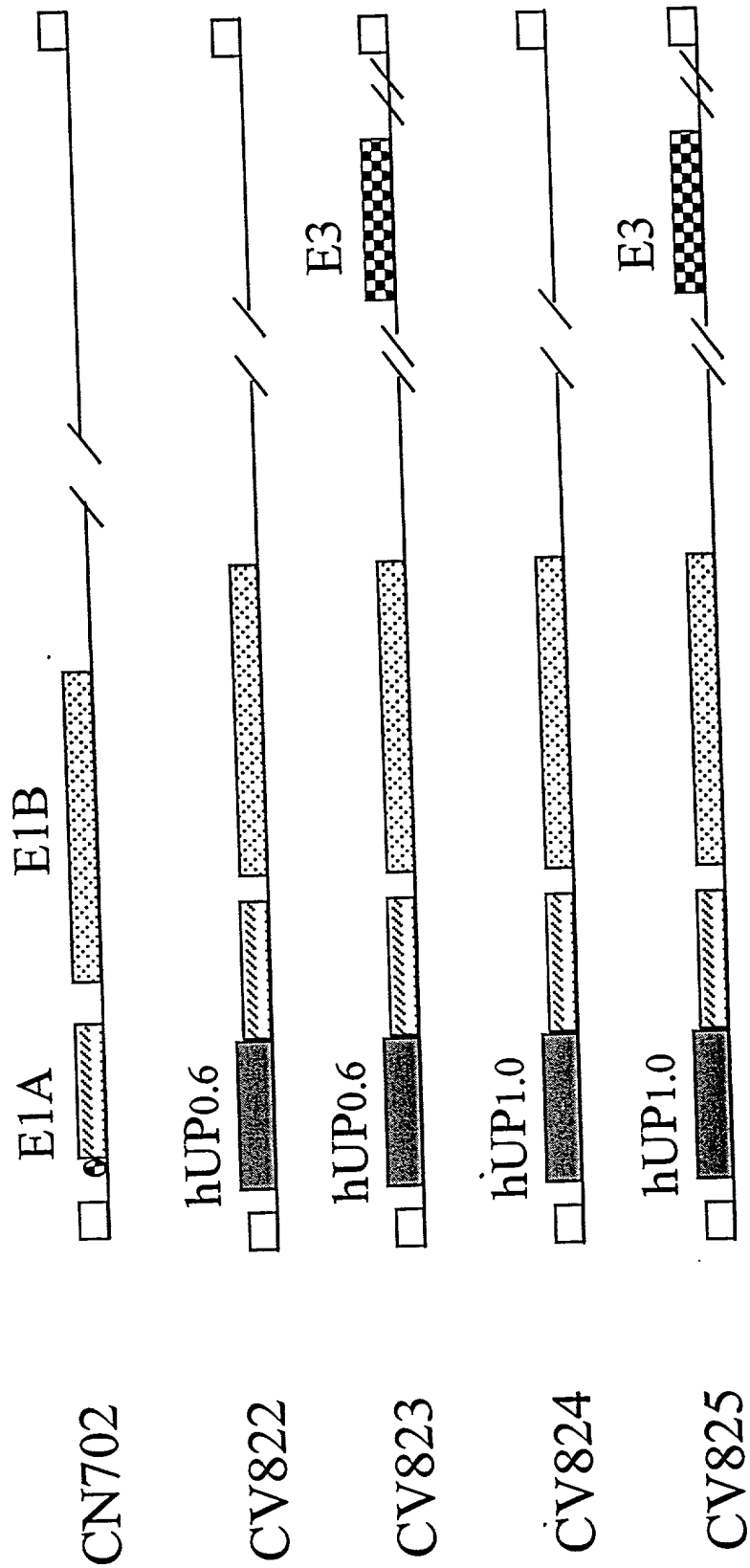


Figure 4C

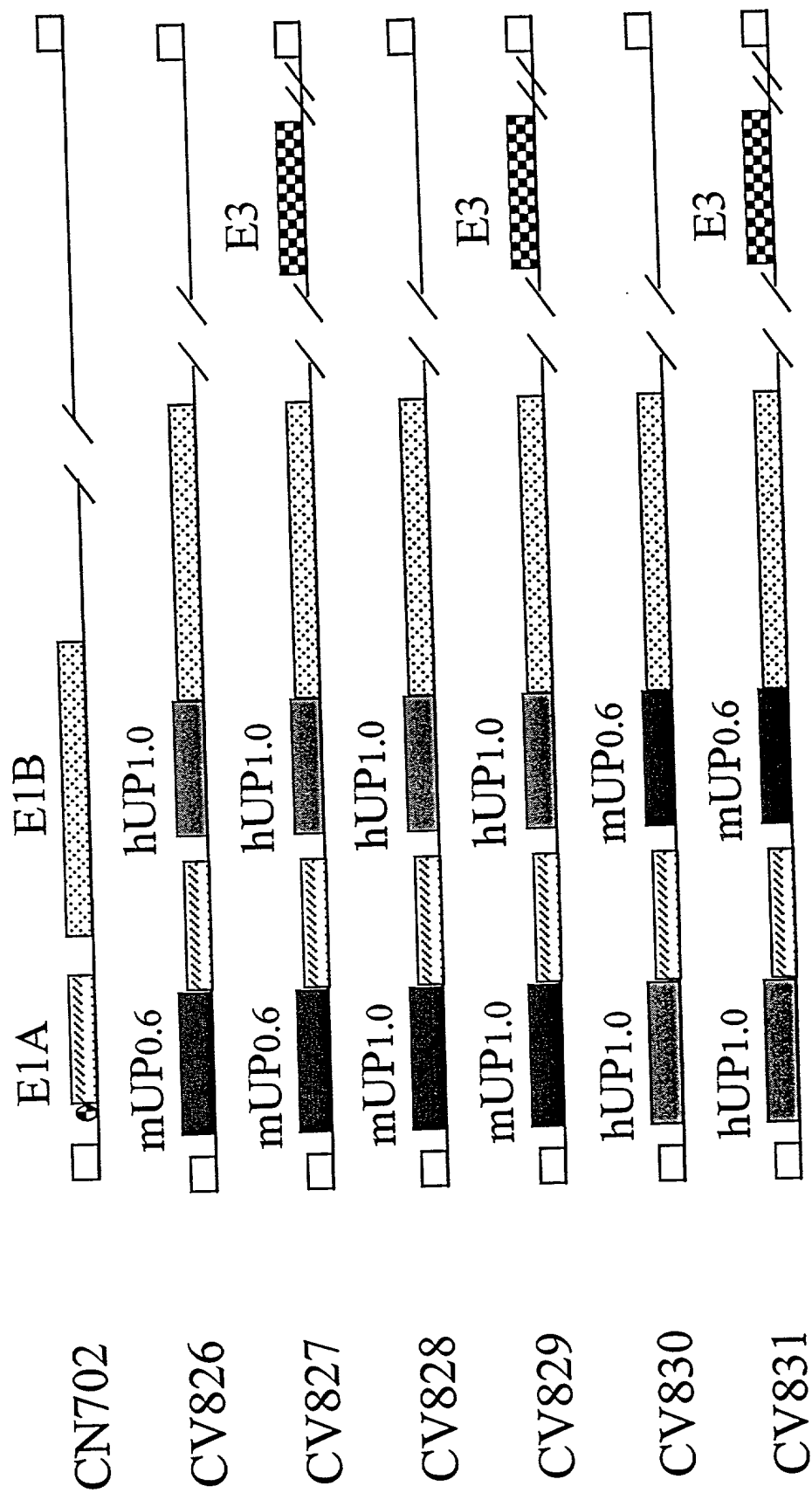


Figure 4D

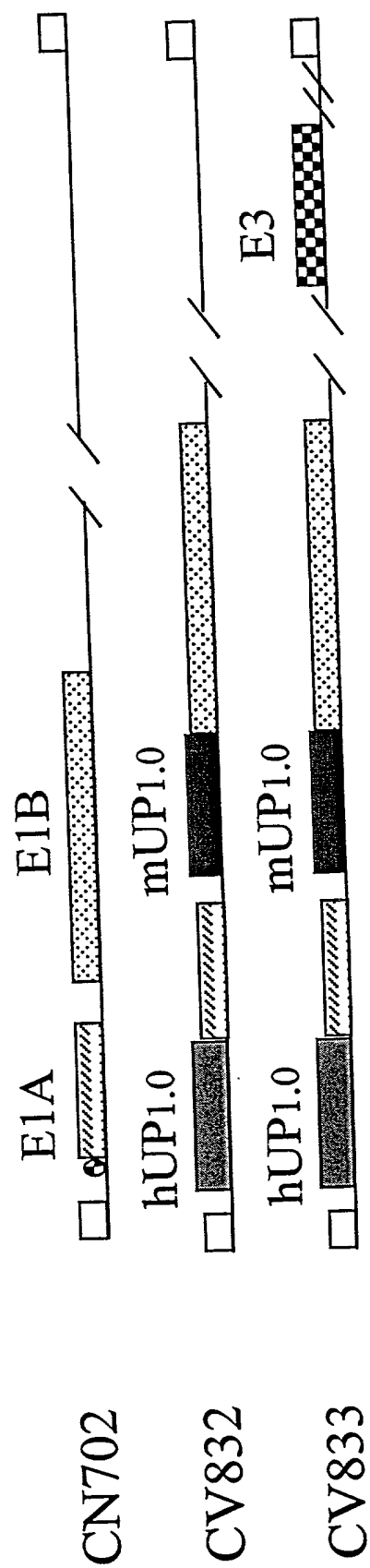


Figure 4E

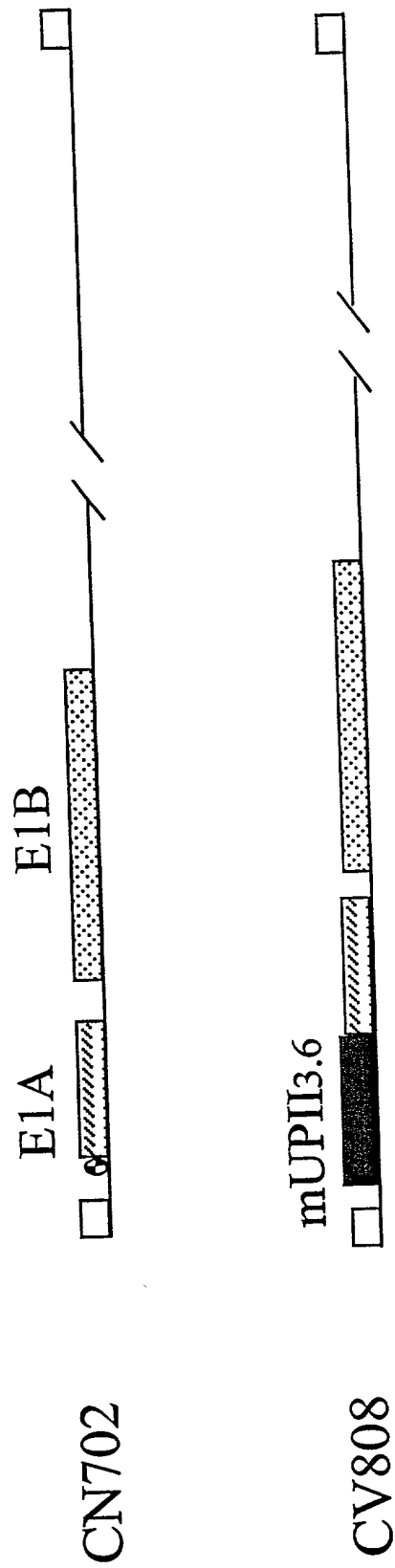


Figure 4F

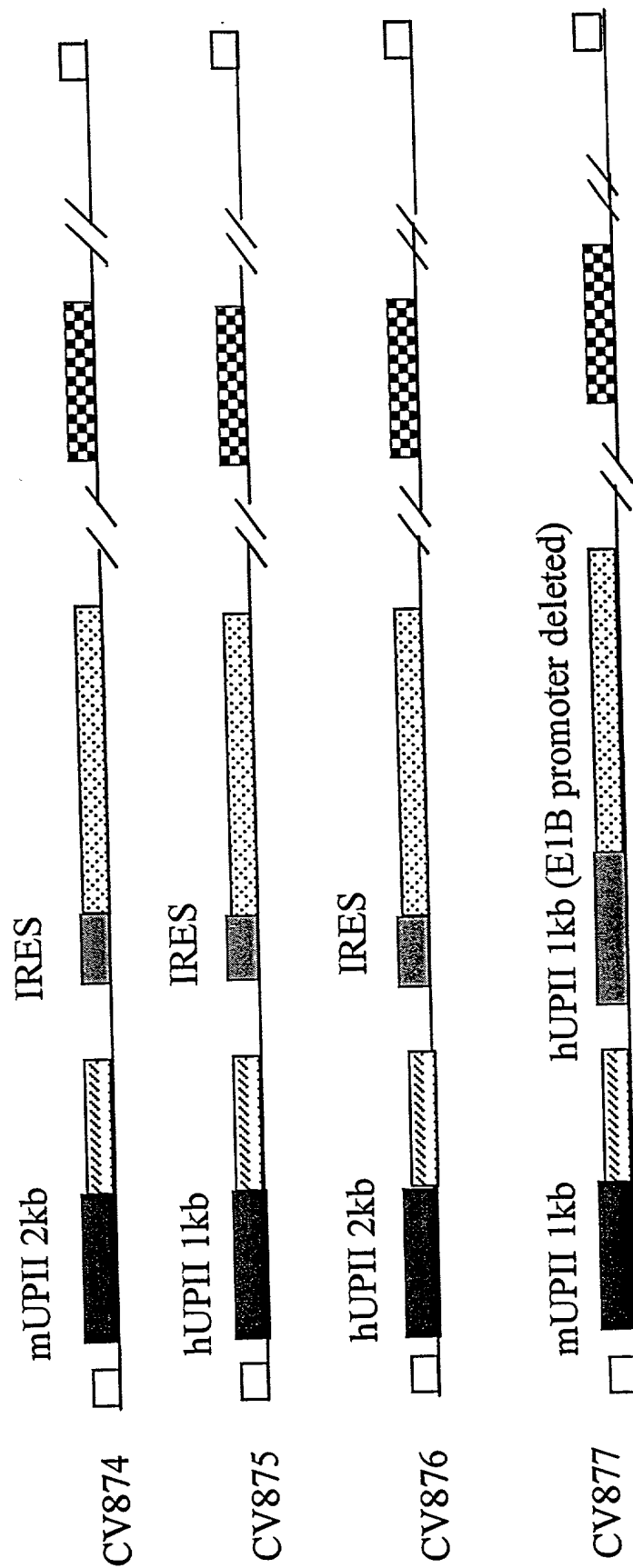
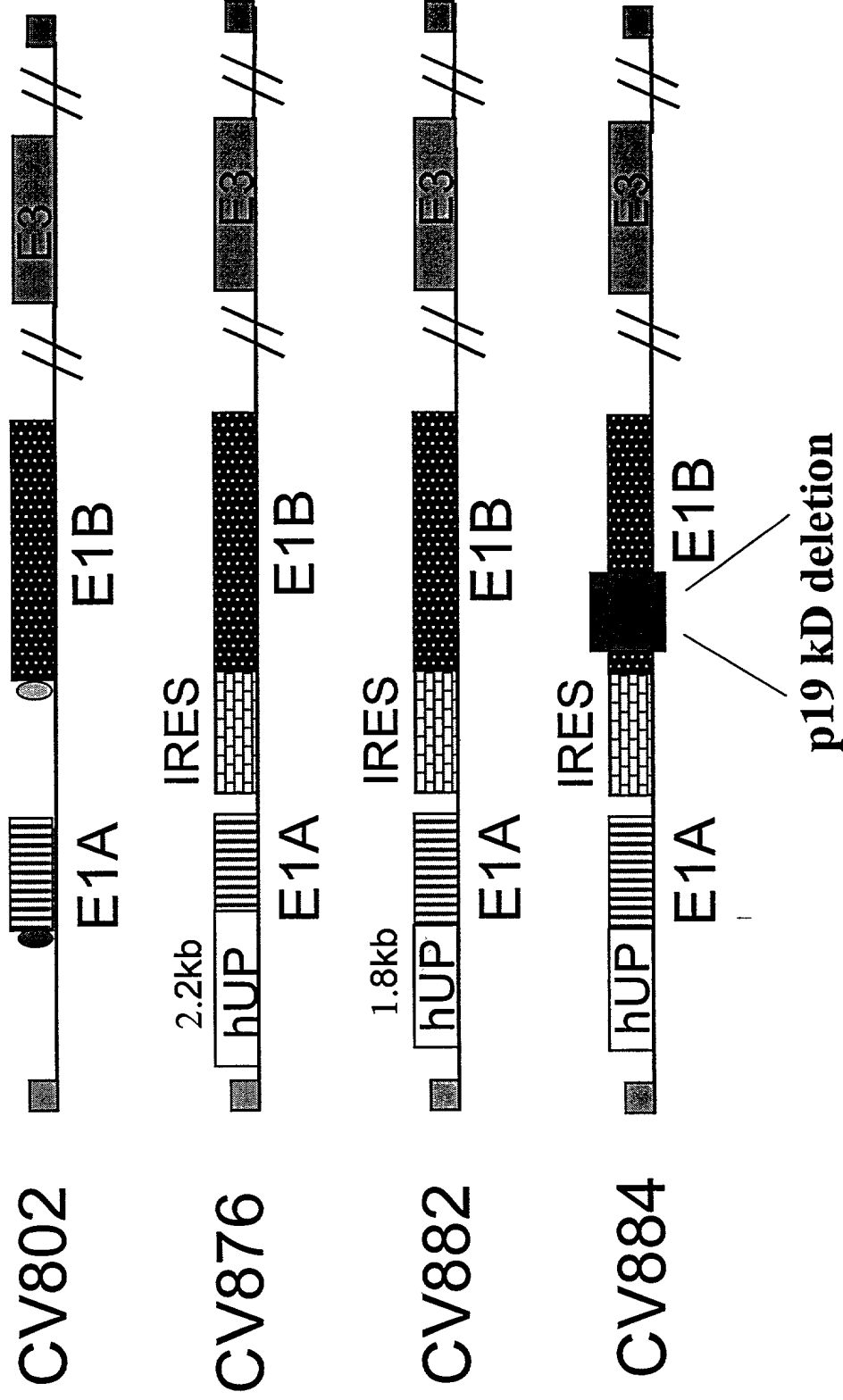


Figure 4G

Structure of CV876, CV882 and CV884



Bladder Specificity of Mouse/Human Uroplakin II promoters

Luciferase Assay

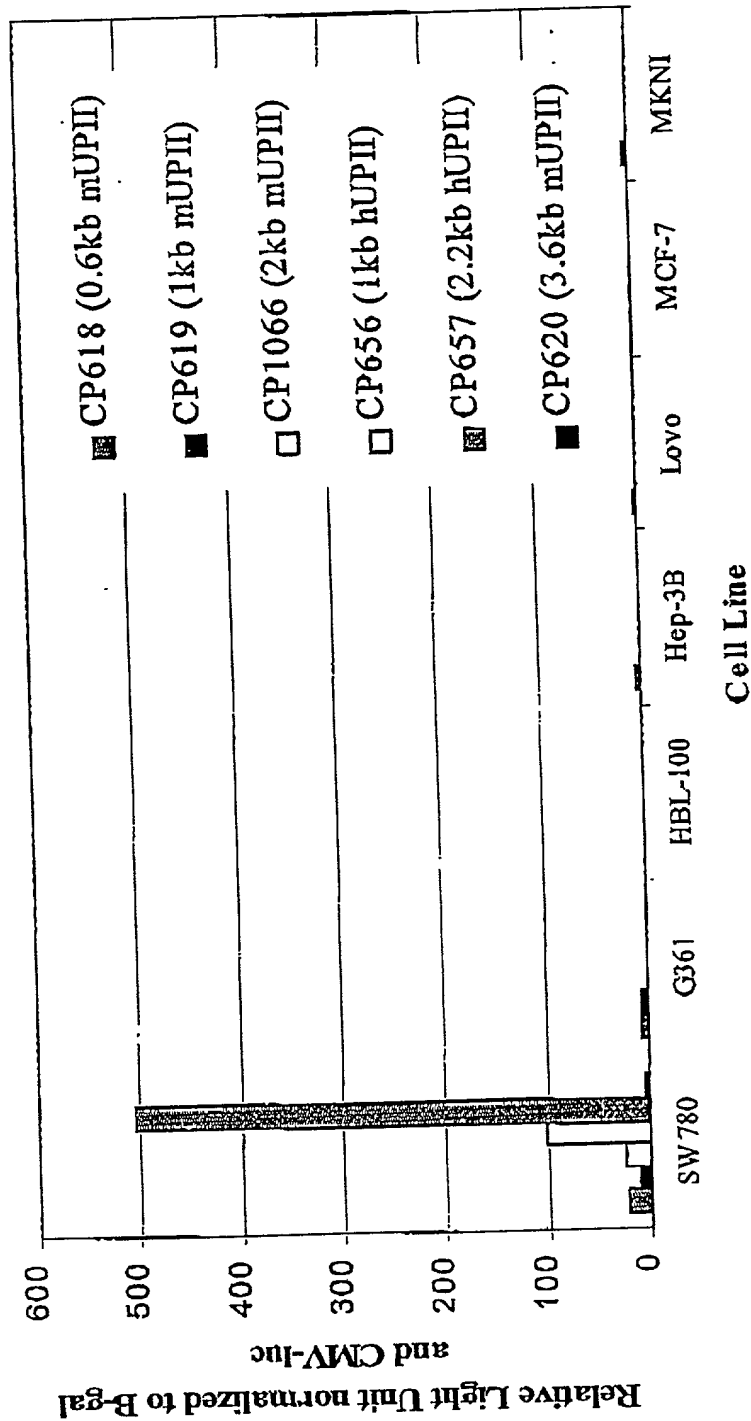


FIG. 7

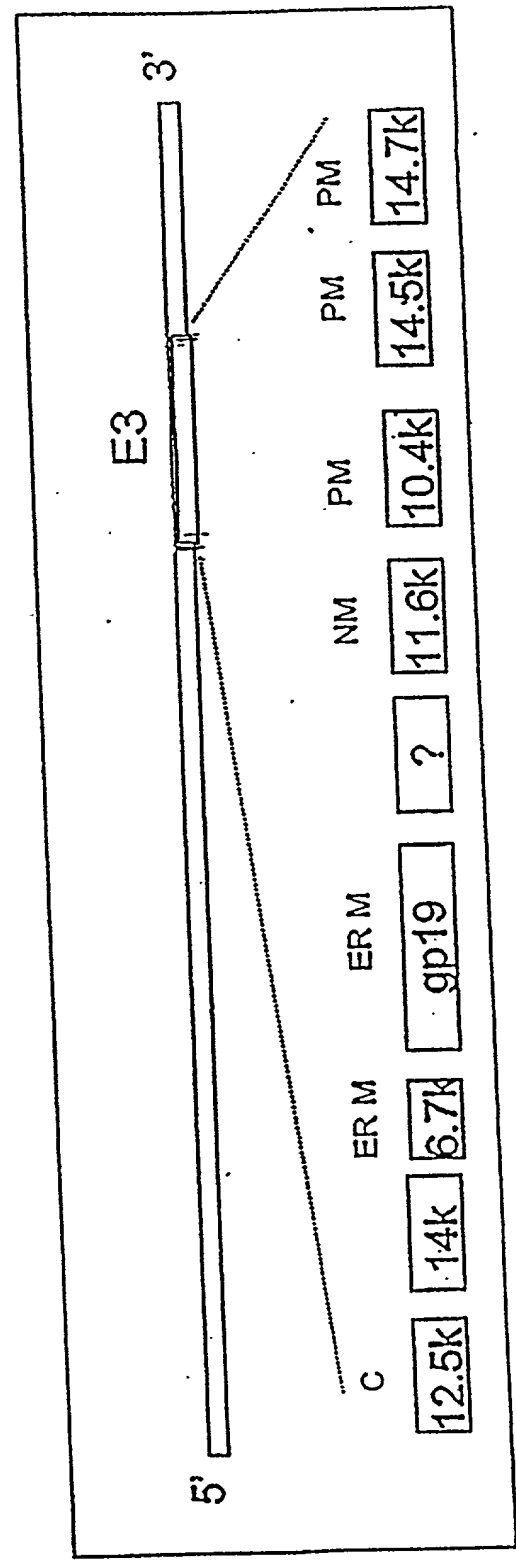


FIG. 9

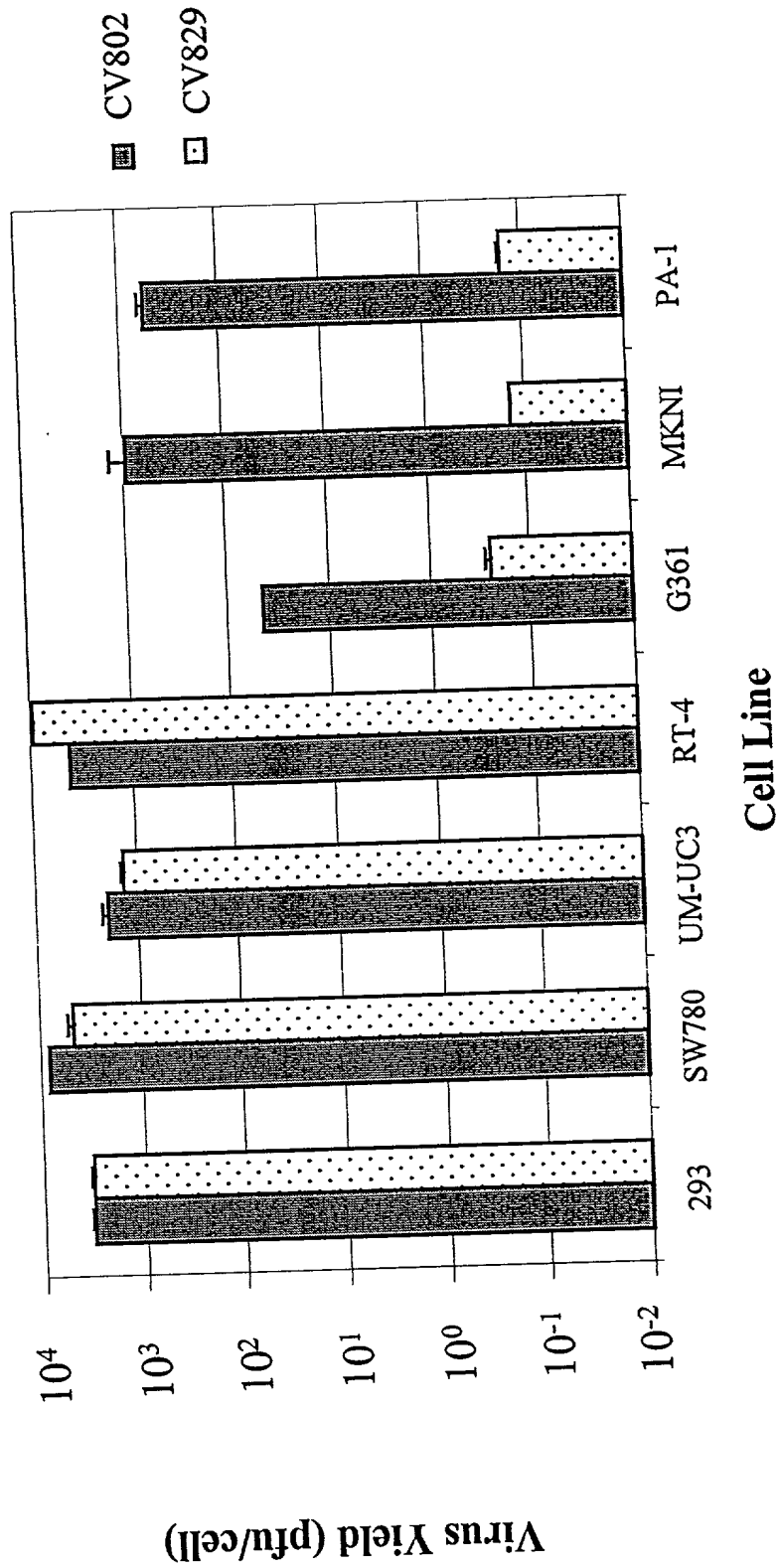


FIG. 10

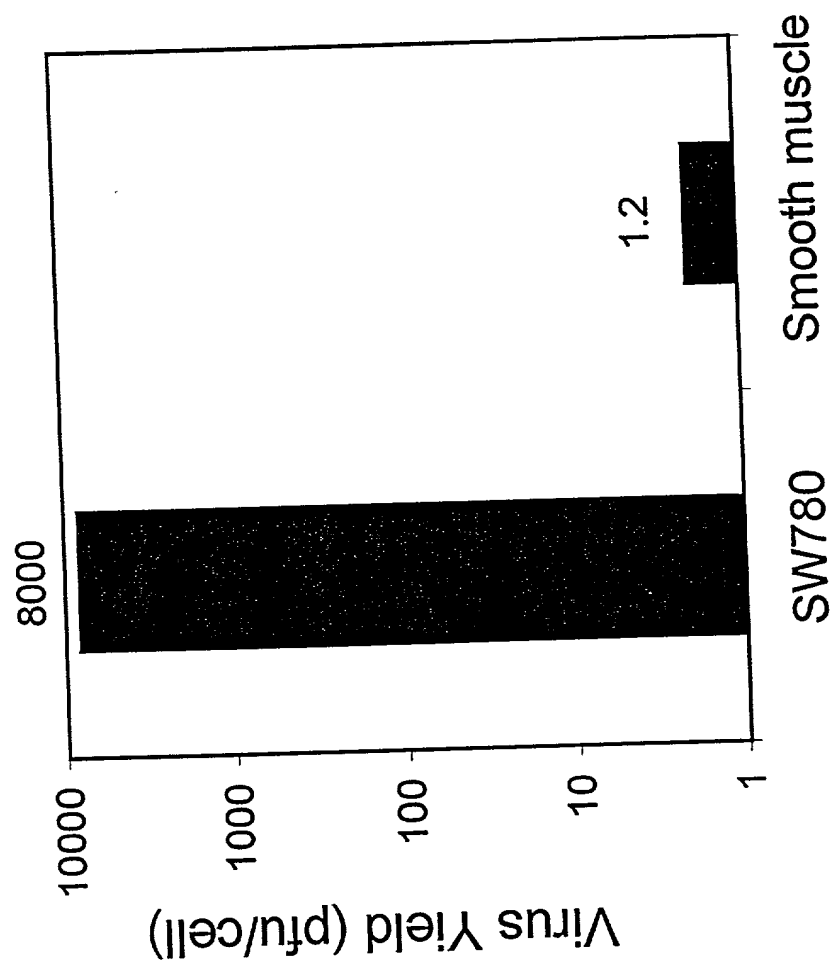


FIG. 11

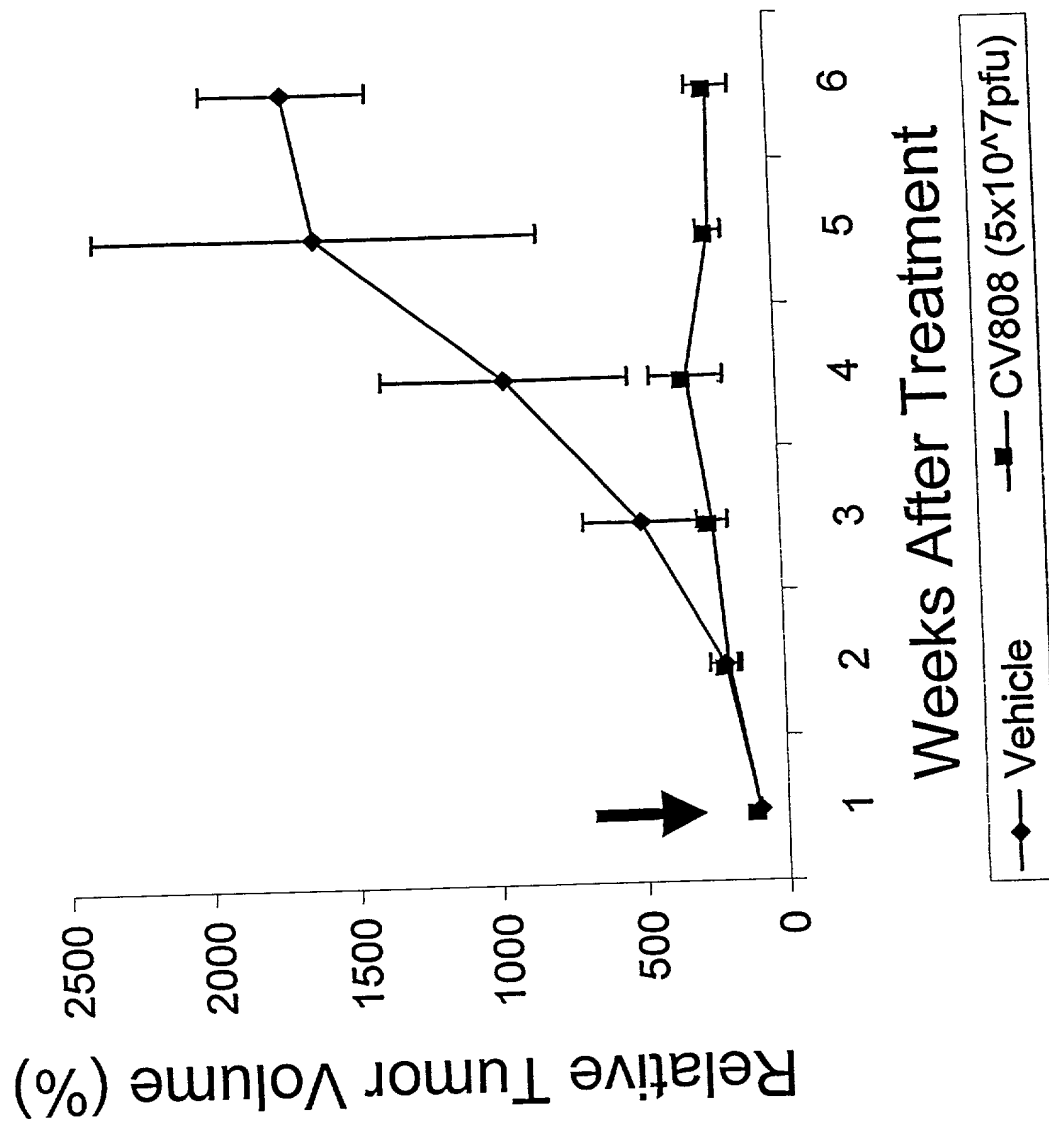


FIG. 12

G ATG ACC GGC TCA ACC ATC GCG CCC ACA ACG GAC TAT CGC AAC ACC
46

Met Thr Gly Ser Thr Ile Ala Pro Thr Thr Asp Tyr Arg Asn Thr
1 5 10 15

ACT GCT ACC GGA CTA ACA TCT GCC CTA AAT TTA CCC CAA GTT CAT GCC
94

Thr Ala Thr Gly Leu Thr Ser Ala Leu Asn Leu Pro Gln Val His Ala
20 25 30

TTT GTC AAT GAC TGG GCG AGC TTG GAC ATG TGG TGG TTT TCC ATA GCG
142

Phe Val Asn Asp Trp Ala Ser Leu Asp Met Trp Trp Phe Ser Ile Ala
35 40 45

CTT ATG TTT GTT TGC CTT ATT ATT ATG TGG CTT ATT TGT TGC CTA AAG
190

Leu Met Phe Val Cys Leu Ile Ile Met Trp Leu Ile Cys Cys Leu Lys
50 55 60

CGC AGA CGC GCC AGA CCC CCC ATC TAT AGG CCT ATC ATT GTG CTC AAC
238

Arg Arg Arg Ala Arg Pro Pro Ile Tyr Arg Pro Ile Ile Val Leu Asn
65 70 75

CCA CAC AAT GAA AAA ATT CAT AGA TTG GAC GGT CTG AAA CCA TGT TCT
286

Pro His Asn Glu Lys Ile His Arg Leu Asp Gly Leu Lys Pro Cys Ser
80 85 90 95

CTT CTT TTA CAG TAT GAT TAA
307

Leu Leu Leu Gln Tyr Asp
100

FIG. 13

Region E3 of Adenovirus

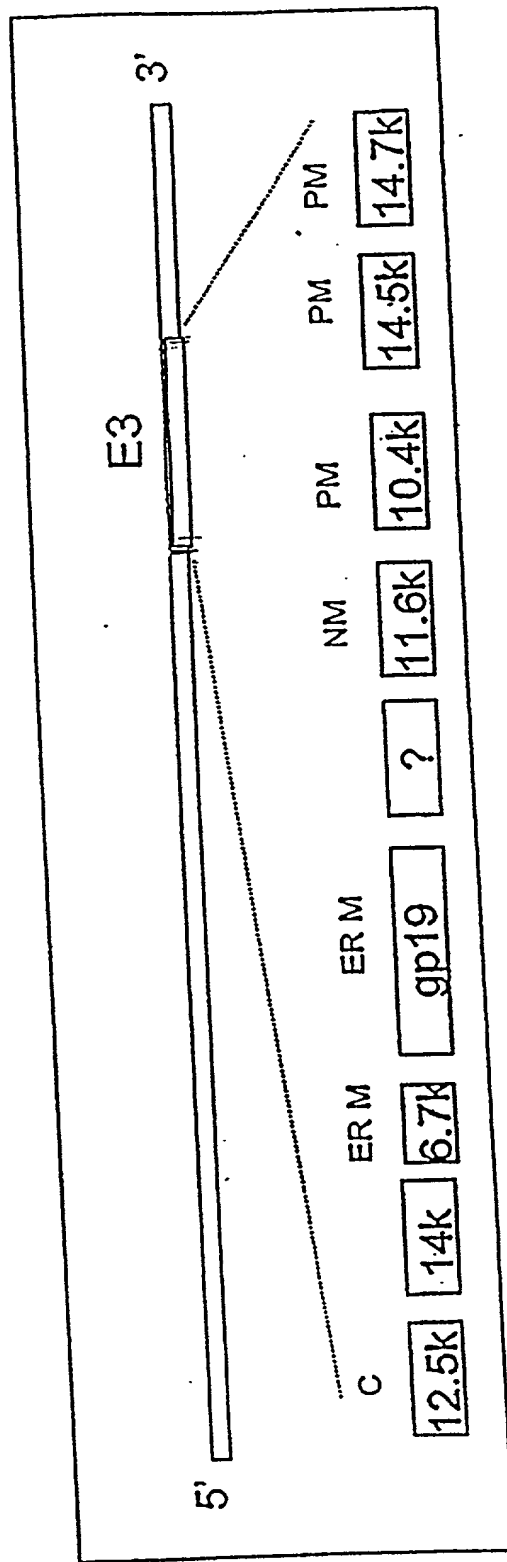


FIG. 14

Virus Yield of CV884

